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121	tgggccttat	atcagtatca	cattgactat	aaccactga	tggaagccag	aagactccgt
181	tcagctcttc	tttttcaaca	cgaagatcta	attggaaagt	gtcatgcttt	tgatggaacg
241	atattatttt	tacctaaaag	actacagcaa	aagggtactg	aagtttttag	taagaccggy
301	aatggagagg	atgtgaggat	aacgatcact	ttaacaaatg	aacttccacc	tacatcacca
361	acttgtttgc	agttctataa	tattattttc	aggaggcttt	tgaaaatcat	gaatttgcaa
421	caaattggac	gaaattatta	taacccaaat	gacccaattg	atattccaag	tcacaggttg
481	gtgatttggc	ctggcttcac	tacttccatc	cttcagtatg	aaaacagcat	catgctctgc
541	actgacgtta	gccataaagt	ccttcgaagt	gagactgttt	tggatttcat	gttcaacttt
601	tatcatcaga	cagaagaaca	taaatttcaa	gaacaagt	ccaaagaact	aataggttta
661	gttgttctta	ccaagtataa	caataagaca	tacagagtgg	atgatattga	ctgggaccag
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1381	caaaagggtca	cagcagacac	ccagatagtt	gtctgtctgt	tgtcaagtaa	tcggaaggac
1441	aaatacagtg	ctattaaaaa	atacctgtgt	acagattgcc	ctaccccaag	tcagtgtgtg
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1861	ggccagctga	aaacactggg	gaactacgaa	gtgccacagt	ttttggattg	tctaaaatcc
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1981	agattttttg	ctcagtctgg	aggaagactt	cagaatccac	ttcctggaac	agttattgat
2041	gtagagggtta	ccagaccaga	atgggtatgac	ttttttatcg	tgagccaggc	tgtgagaagt
2101	ggtagtggtt	ctccacacaca	ttacaatgtc	atctatgaca	acagcggcct	gaagccagac
2161	cacatacagc	gcttgaccta	caagctgtgc	cacatctatt	acaactggcc	aggtgtcatt
2221	cgtgttcctg	ctccttgcca	gtacgcccac	aagctggctt	ttcttggttg	ccagagtatt
2281	cacagagagc	caaactctgtc	actgtcaaac	cgcctttact	acctctaa	

Figure 1

Met Ile Phe Gly Val Asn Thr Arg Gln Asn Leu Asp His Val Lys Glu Ser Lys Thr Gly Ser Ser Gly Ile Ile Val Arg Leu Ser Thr 30
 Asn His Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg 60
 Ser Ala Leu Leu Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln 90
 Lys Val Thr Glu Val Phe Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr Asn Glu Leu Pro Thr Ser Pro 120
 Thr Cys Leu Gln Phe Tyr Asn Ile Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Gln Ile Gly Arg Asn Tyr Tyr Asn Pro Asn 150
 Asp Pro Ile Asp Ile Pro Ser His Arg Leu Val Ile Trp Pro Gly Phe Thr Thr Ser Ile Leu Gln Tyr Glu Asn Ser Ile Met Leu Cys 180
 Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu His Lys Phe Gln 210
 Glu Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln 240
 Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe Leu Glu Tyr Tyr Arg Lys Lys Gln Tyr Asn Gln Glu Ile Thr Asp 270
 Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu 300
 Cys Tyr Leu Thr Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu Ala Val His Thr Arg Leu Thr Pro Glu Gln 330
 Arg Gln Arg Glu Val Gly Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu Arg Asp Trp Gly Leu Ser Phe Asp 360
 Ser Asn Leu Leu Ser Phe Ser Gly Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala 390
 Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg Arg Asn Tyr Glu 420
 Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val Asp Asp 450
 Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp 480
 Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr 510

Figure 1
Continued

Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val 540

Met Ile Val Gly Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr 570

Arg Trp Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp 600

Asn Ser Cys Asn Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu 630

Val Pro Gln Phe Leu Asp Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys Arg Val Asn Thr 660

Arg Phe Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr Arg Pro Glu Trp Tyr Asp 690

Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu Lys Pro Asp 720

His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala His 750

Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn Leu Ser Asn Arg Leu Tyr Tyr Leu 775

Figure 1
Continued

PIWI MADDQGRGRRRPLNEDDSSTSRGSGDGPVKVFRGSSSGDPRADPRIEASRERRALEEAPR
 M F G R L 61
 HIWI M-----IF-----G-----VNTRQNLHDV--

 PIWI REGGPPERKPGWDQYDYLNTFRVELVSKKGTGVPVMLQTNFFRLKTKPEWRIVHYHVEFE
 K E SK G+ G+ V L TN FRL ++P+W + YH+++ 122
 HIWI -----K-----E--SKTGSSGIIVRLSTNHFRLTSRPQWALYQYHIDYN

 PIWI PSIENPRVRMGVLSNHANLLGSGYLFDFGLQFTTRKFEQETVLSGKSKLDIEYKISIKFV
 P +E R+R +L H +L+G + FDG LF ++ +Q++T + K++ + +I+I 183
 HIWI PLMEARRLRALLFQHEDLIGKCHAFDGTILFLPKRLQQKVTEVFSKTRNGEDVTRITITLT

 PIWI GFISCAEPFLQVLNLILRRSMKGLNLELVGRNLFDPRAKIEIREFKMELWPGYETSIRQH
 + P LQ N+I RR +K +NL+ +GRN ++P I+I ++ +WPG+ TSI Q+ 244
 HIWI NELPPTSPTCLQFYNIIFRRLKIMNLQQIGRNYNPNNDPIDIPSHRLVIWPGFTTSLQY

 PIWI EKDILLGTEITHKVMRTETIYDIMRRCSHNPARH--QDEV RVNVL DLIVLTDYNNRTYRIN
 E I+L T+++HKV+R+ET+ D M H H Q++V ++ L+VLT YNN+TYR++ 305
 HIWI ENSIMLCTDVSHKVLRSFVLD FMFNFYHQTEEHKFQEQVSKELIGLVLT KYNNKTYRVD

 PIWI DVDFGQTPKSTF-SCKGRDISFVEYYLT KYNIRIRDHNQPLLISK-NRDKALKTNASELVV
 D+D+ Q PKSTF G ++SF+EYY +YN I D QP+L+S+ R + + 366
 HIWI DIDWDQNPKSTFKKADGSEVSFLEYRQYNOEITDLKQPVLSQPKRRRGPGGTLPGPAM

 PIWI LIPELCRVLTGLNAEMRSNFQMLRAMSSYTRMNPQR---TDRLRAFNRHLQNTPESVKVL R
 LIPELC +TGL +MR++F +M+ ++ +TR+ P+QR RL + H+ N LR 427
 HIWI LIPELCYLTGLTDKMRNDFNVMKDLAVHTRLTPEQRQREVGRLLIDYIHKNDNVQ---REL R

 PIWI DWNMELDKNVTEVQGRIGQQNIVFHNGKVPAGEN---ADWQRHFRDQRMLTTPSDGLDRW
 DW + D N+ GRI+ + I H G N ADW + R +++ LD W 488
 HIWI DWGLSFDSNLLSFSGRILQTEKI--HQGGKTFDYNPQFADWSKETRGAPLISVKP--LDNW

 PIWI AVIAPQRNSHELRTLLDSLYRAASGMGLRIRSPQEFIIYDDRTGTYVRAMDDCVRSDPKLI
 +I +RN +L+ +L++ MG+++R I DDRT Y+R + V +D++++ 549
 HIWI LLIYTRRNYEAANS LIQNLFKVTPAMGMQMRK-AIMIEVDDRTEAYLRVLQKVTADTQIV

 PIWI LCLVPNDNAERYSSIKKRGYVDRAVPTQVVT LKTTKKPYSLMSIATKIAIQLNCKLGYTPW
 CL+ ++ ++Y +IKK D P+Q V +T K ++M+IATKIA+Q+NCK+G W 610
 HIWI VCLLSSNRKDKYDAIKKYLCTDCPTPSQCVVARTLGKQQTVMATKIALQMNCKMGGELW

 PIWI MIELPLSGLMTIGFDIAKSTRDRKRAYGALIASMDLQQNSTYFSTVTECSAFDVLANTLWP
 +++PL +M +G D +R+ +AS++ + + +FS L+ L 671
 HIWI RVDIPLKLVMI VGIDCYHDMTAGRRSIAGFVASIN-EGMTRWFSRCIFQDRGQELVDGLKV

 PIWI MIAKALRQYQHEHRKLPSRIVFYRDGVSSGSLKQLFEFEVKDII EKLT EYARVQLSPPQL
 + ALR + + +PSRI+ YRDGV G LK L +EV ++ LK+ P+L 732
 HIWI CLQAALRAWNSCNEYMPRIIVYRDGVGDGQLKTLVNYEVPQFLDCLKSIGRGYN---PRL

 PIWI AYIVVTRSMNTRFFLNG----QNPPPGTIVDDVITLPERYDFYLSQQVRQGTVSPTSYNV
 IVV + +NTRFF QNP PGT++D +T PE YDF++VSQ VR G+VSPT YNV 793
 HIWI TVIVVKRVNTRFFAQSGGRLQNPLPCTVIDVEVTRPEWYDFFIVSQAVRSGSVSPHYNV

 PIWI LYSSMGLSPEKMQLTYKMCHLYYNWSGTTRVPAVCQYAKKLATLVGTNLHSIPQNALEK
 +Y + GL P+ +Q+LTYK+CH+YYNW G RVPA CQYA KLA LVG ++H P +L 854
 HIWI IYDNSGLKPDHIQRLTYKLCHIIYNWPGVIRVPAPCQYAHKLAFLVGQSIHREP NLSLSN

 PIWI KFYYL
 + YYL 859
 HIWI RLYYL

Figure 1
Continued

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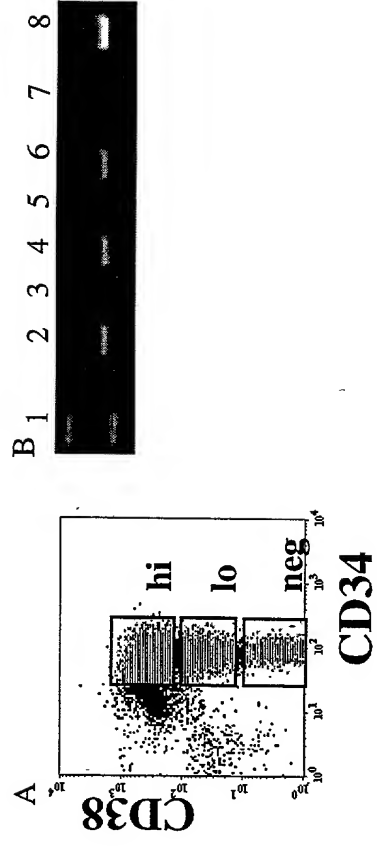


Figure 2

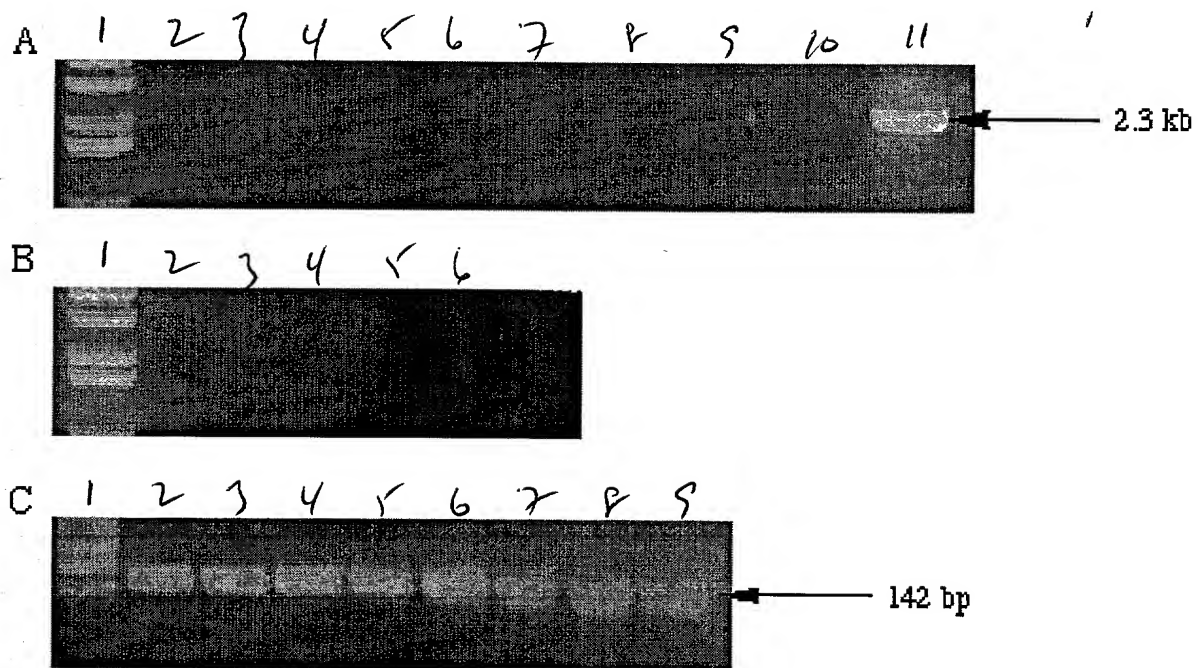


Figure 3

2007-10-4/24007

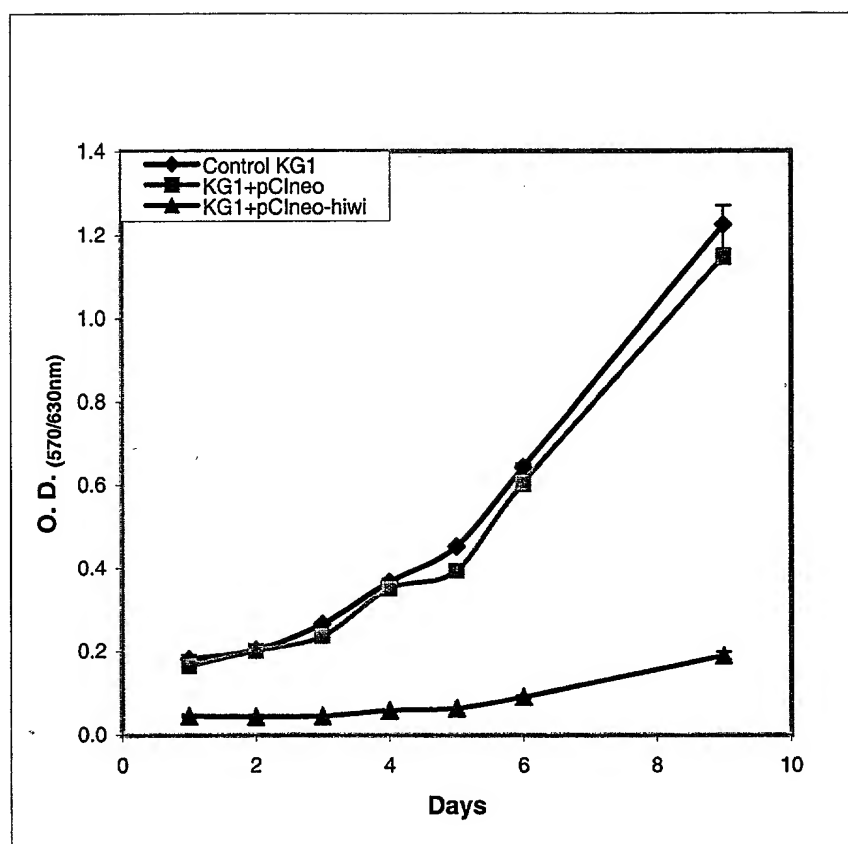


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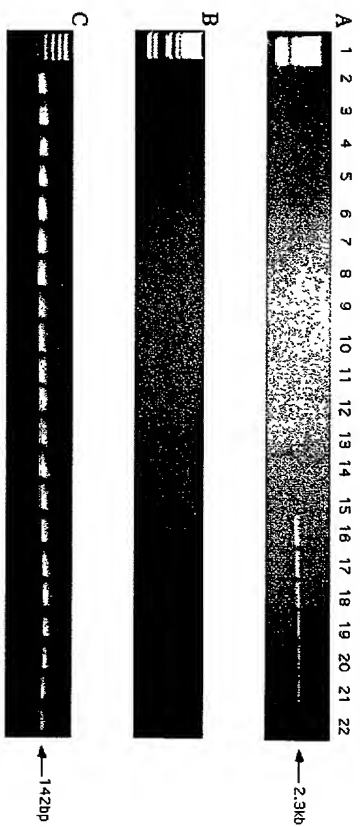
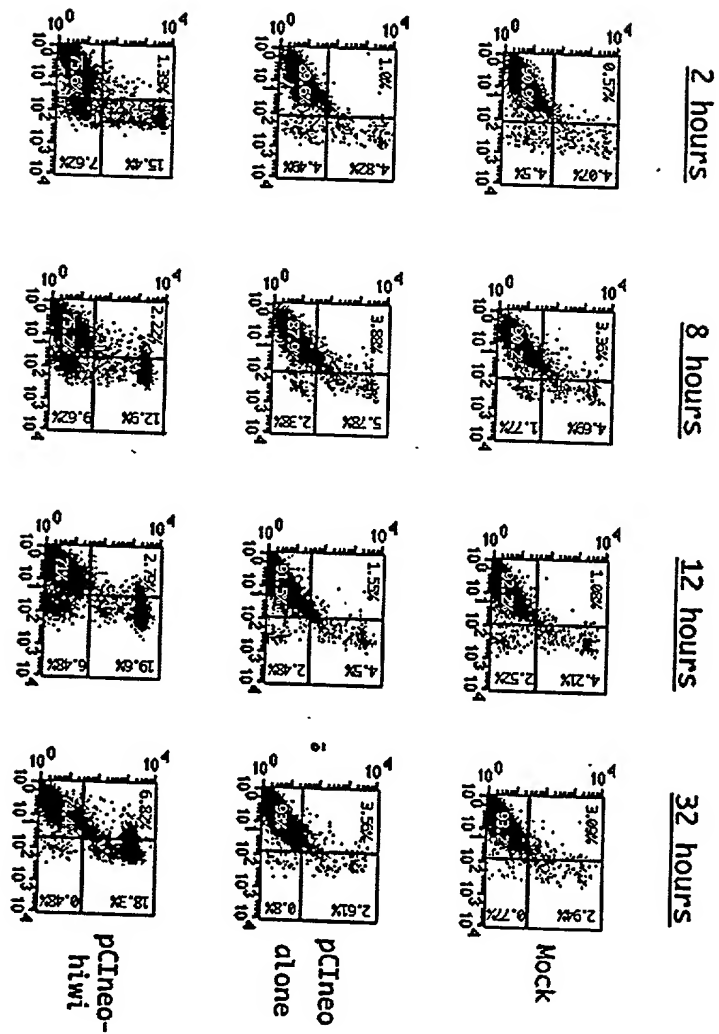


Figure 5

1004374.01.002

Propidium Iodide



Annexin V

Figure 6

B



1 Kb Ladder
Heart
Brain
Kidney
Liver
Lung
Skeletal muscle
Thymus
Prostate
Testis
Leukocyte
Ovary
Small intestine
Placenta
Pancreas
Water control
1 Kb Ladder

A



1 Kb Ladder
Heart
Brain
Kidney
Liver
Lung
Skeletal muscle
Spleen
Thymus
Water control
1 Kb Ladder

Figure 7

1004374.01.1002

200T10-42E400T

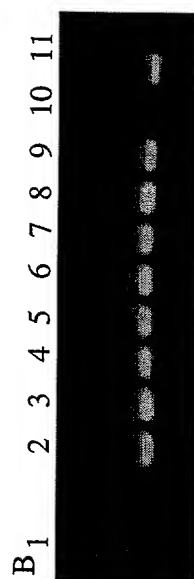


Figure 8

1004374-011002

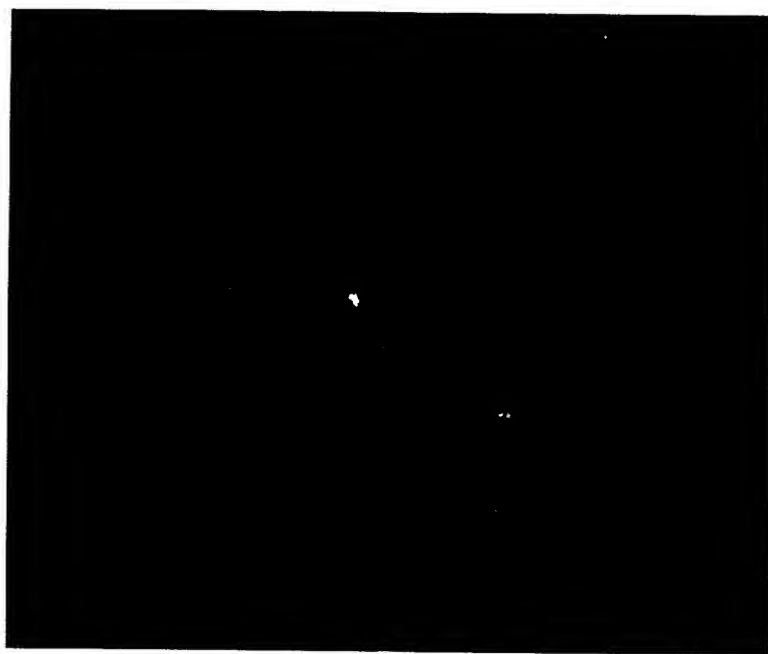
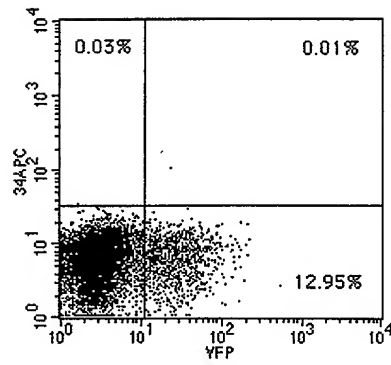
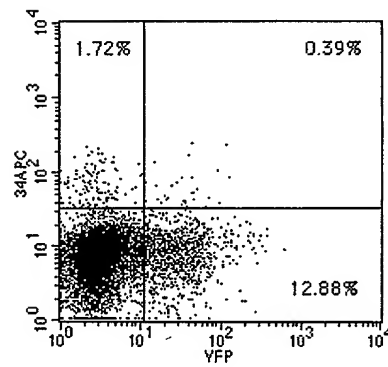


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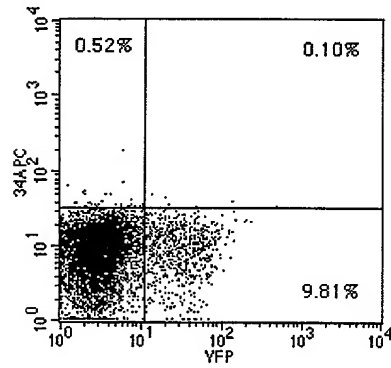
Hiwi Isotype Control



Hiwi CD34/YFP



Empty Vector Isotype Control



Empty Vector CD34/YFP

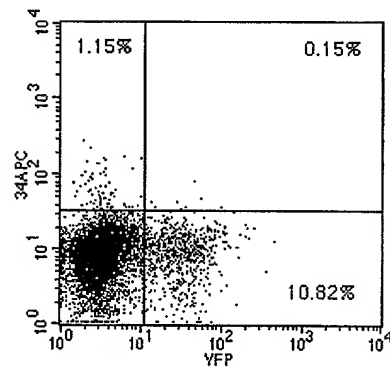


Figure 10